

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Novel elongase gene and process for the production
of polyunsaturated fatty acids

<130> 925_2001

<140>

<141>

<160> 2

<170> PatentIn Vers. 2.0

<210> 1

<211> 1066

<212> DNA

<213> Phytophthora infestans

<220>

<221> CDS

<222> (52)..(888)

<400> 1

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gaattcggca cgaggttcgc acgtccatcg tctactcacc aacaagaagt c atg tcg 57
                                     Met Ser
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act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg gag gcc 105
Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr Glu Ala
      5                      10                      15

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aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg cat cct 153
Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val His Pro
      20                      25                      30

```

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atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc atc tgc 201
Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala Ile Cys
      35                      40                      45                      50

```

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gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg aaa atg 249
Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met Lys Met
      55                      60                      65

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gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac aac ccc 297
Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr Asn Pro
      70                      75                      80

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atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc atc cag 345
Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala Ile Gln
      85                      90                      95

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gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt aag tcc 393
Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe Lys Ser
      100                      105                      110

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gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc tcc aag 441
 Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu Ser Lys
 115 120 125 130

atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag aag tgg 489
 Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys Lys Trp
 135 140 145

aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg ctt ttc 537
 Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val Leu Phe
 150 155 160

gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca tat gct 585
 Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser Tyr Ala
 165 170 175

acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act tac tac 633
 Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr Tyr Tyr
 180 185 190

ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac ctc acg 681
 Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr Leu Thr
 195 200 205 210

cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc tac ctg 729
 Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly Tyr Leu
 215 220 225

acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg ctc atg 777
 Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro Leu Met
 230 235 240

tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat ttc tac 825
 Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn Phe Tyr
 245 250 255

att cgc gcg tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag gaa tcg 873
 Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu Glu Ser
 260 265 270

aag aag aag ttg taa cggcgcttgt taaaaagtct aacctcgctg taacagctta 928
 Lys Lys Lys Leu
 275

aaacacacac acacacaacg cttttagtag gaggtaagta gtggcaactc gtgtagaaat 988

gcagcatgcc catcaaatac atcccgtatg attcaaaaaa aaaaaaaaaa aaaaaaaaaa 1048

aaaaaaaaaa aactcgag 1066

<210> 2
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 <212> PRT
 <213> *Phytophthora infestans*

<400> 2

Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr
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Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val
 20 25 30

His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala
 35 40 45

Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met
 50 55 60

Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr
 65 70 75 80

Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala
 85 90 95

Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe
 100 105 110

Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu
 115 120 125

Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys
 130 135 140

Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val
 145 150 155 160

Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser
 165 170 175

Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr
 180 185 190

Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr
 195 200 205

Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly
 210 215 220

Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro
 225 230 235 240

Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn
 245 250 255

Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu
 260 265 270

Glu Ser Lys Lys Lys Leu
 275